

DOI: 10.1002/cmdc.200600115

Probing, Inhibition, and Crystallographic Characterization of Metallo- β -lactamase (IMP-1) with Fluorescent Agents Containing Dansyl and Thiol Groups

Hiromasa Kurosaki,^{*[a]} Yoshihiro Yamaguchi,^{*[b]} Hisami Yasuzawa,^[a] Wanchun Jin,^[a] Yuriko Yamagata,^[c] and Yoshichika Arakawa^[d]

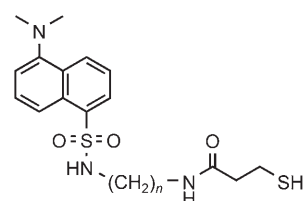
The treatment of bacterial infections has advanced rapidly in recent years, primarily as the result of the development of multiple antibacterial agents.^[1–3] However, with the widespread use of such antibacterial agents, various pathogens have developed a resistance to antibiotics and are now a global problem as nosocomial pathogens in immunocompromised patients.^[4] One of the mechanisms of bacterial resistance is the production of enzymes that render drugs inactive.^[5] For example, β -lactamases, produced by various pathogenic bacteria, catalyze the hydrolysis of the β -lactam ring of β -lactam antibiotics.^[6–9]

β -Lactamases can be classified into four molecular classes: A, B, C, and D.^[10,11] β -Lactamases in classes A, C, and D are serine enzymes with a serine residue at the active site, whereas class B β -lactamases require divalent metal ions such as Zn^{II}, and are referred to as the metallo- β -lactamases (MBLs).^[6–9] MBLs are able to hydrolyze nearly all β -lactam antibiotics, including carbapenems, and are also generally not susceptible to β -lactamase inhibitors such as clavulanic acid, tazobactam, and sulbactam, which are routinely used for clinical treatment.^[12]

Among the most widely recognized MBLs, IMP-1 is extremely widespread. The resistance gene, *bla*_{IMP} is included in an in-

tegron structure that is present in the mobile plasmid as a cassette.^[13] Therefore, it is possible for the gene to horizontally propagate to other bacteria, and the isolation of IMP-1 has been reported in both Japan and Europe.^[14] The rampancy of pathogenic bacteria that retain IMP-1 is due to the fact that it efficiently hydrolyzes carbapenems, unlike the class A, C, and D β -lactamases. Thus, it is very important to confirm the production of IMP-1 in infectious bacteria for effective chemotherapy at the initial stages of a disease.

We are currently in the process of developing reagents for IMP-1 detection based on the use of a fluorescent probe. We recently reported that thiocarboxylic acid derivatives inhibit IMP-1, reversibly or irreversibly.^[15–17] We have also reported on a fluorescent probe for detecting IMP-1, *N*-(5-(dimethylamino)-1-naphthalenesulfonamidoethyl)-3-thiopropionamide, (Dansyl-C₂SH, Figure 1).^[18] A compound containing a thiol group as a



$n = 2$: DansylC₂SH; $n = 3$: DansylC₃SH;
 $n = 4$: DansylC₄SH; $n = 5$: DansylC₅SH;
 $n = 6$: DansylC₆SH

Figure 1. Structures of DansylC_nSHs ($n = 2–6$).

Zn^{II} ligand and a dansyl group as a fluorophore would be expected to serve as an effective fluorescent probe for detecting IMP-1. Moreover, in an attempt to optimize its fluorescence properties, we designed some new fluorescence probes, DansylC_nSHs ($n = 2–6$, Figure 1) in which the length of the methylene chain between the dansyl and thiol groups is varied.

Herein, we describe the synthesis, fluorescence properties, and inhibition activities of DansylC_nSHs with IMP-1. We also determined the X-ray crystal structure of IMP-1 complexed with DansylC₄SH, which, of the DansylC_nSHs examined to date, is the most highly sensitive fluorescent probe and an inhibitor of IMP-1. By connecting the dansyl and 3-thiopropionic acid groups with linkers of various length, the ability to detect and evaluate the inhibition activity of MBLs such as IMP-1,^[13] VIM-2,^[19] and variants thereof^[20–23] can be tuned.

The fluorescent DansylC_nSH probes were synthesized in one-step reactions in 31–77% yield by condensing 3-thiopropionic acid with *N*-(aminoalkyl)-5-dimethylaminonaphthalene-1-sulfonamide using *N,N'*-dicyclohexylcarbodiimide followed by silica gel column chromatography (see Supporting Information).

We examined the ability of the fluorescent agent to detect IMP-1 by measurement of the fluorescence emission spectra ($\lambda_{\text{excitation}} = 340$ nm) of 1 μM DansylC_nSHs with varying concentrations of IMP-1 (0–10 μM) in 50 mM Tris-HCl buffer (pH 7.4) containing 0.5 M NaCl and 10% methanol. As the concentration of IMP-1 increased, the fluorescence emission intensity of

[a] Dr. H. Kurosaki, H. Yasuzawa, W. Jin
 Department of Structure–function Physical Chemistry
 Graduate School of Pharmaceutical Sciences
 Kumamoto University
 Oe-honmachi 5-1, Kumamoto 862-0973 (Japan)
 Fax: (+81) 96-371-4314
 E-mail: ayasaya@gpo.kumamoto-u.ac.jp

[b] Dr. Y. Yamaguchi
 Environmental Safety Center
 Kumamoto University
 39-1, Kurokami 2-Chome, Kumamoto 860-8555 (Japan)
 Fax: (+81) 96-342-3238
 E-mail: yyamagu@gpo.kumamoto-u.ac.jp

[c] Prof. Dr. Y. Yamagata
 Department of Structural Biology
 Graduate School of Pharmaceutical Sciences
 Kumamoto University
 Oe-honmachi 5-1, Kumamoto 862-0973 (Japan)

[d] Director. Dr. MD Y. Arakawa
 Department of Bacterial Pathogenesis and Infection Control
 National Institute of Infectious Diseases
 4-7-1 Gakuen, Musashi-Murayama, Tokyo 208-0011 (Japan)

Supporting information for this article is available on the WWW under <http://www.chemmedchem.org> or from the author.

the DansylC_nSHs also increased, and the fluorescence emission maxima were shifted to a shorter wavelength (Figure 2a–e), indicating that DansylC₄SH is the most blue-shifted amongst the DansylC_nSHs used in this study. At a concentration of 1 μM IMP-1, the ratios of the fluorescence intensities of 1 μM DansylC_nSHs in the presence and absence of 1 μM IMP-1 at $\lambda = 535$ nm were 3.0 for $n=2$, 2.8 for $n=3$, 5.9 for $n=4$, 3.6 for $n=5$, and 3.5 for $n=6$.

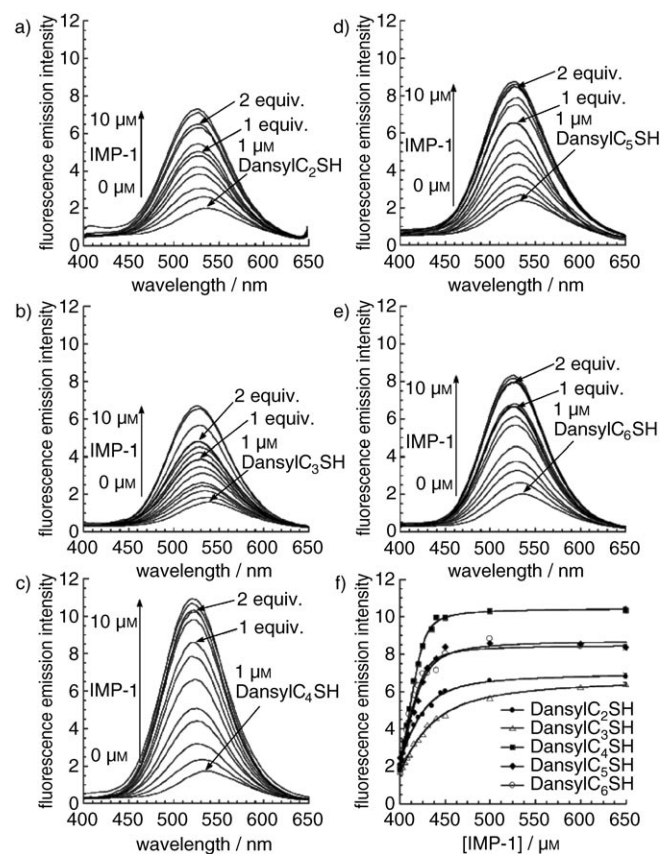


Figure 2. Fluorescence emission spectra ($\lambda_{\text{excitation}} = 340$ nm) of 1 μM DansylC_nSHs ($n = 2-6$) with increasing concentrations of IMP-1 ranging from 0 to 10 μM : a) DansylC₂SH; b) DansylC₃SH; c) DansylC₄SH; d) DansylC₅SH; e) DansylC₆SH. These spectra were measured at 25 °C in 50 mM Tris-HCl buffer (pH 7.4) containing 0.5 M NaCl and 10% methanol. f) Fluorescence emission intensity as a function of the concentration of added IMP-1 monitored at $\lambda = 535$ nm. The apparent dissociation constants of each DansylC_nSH with IMP-1 were analyzed from the data by nonlinear least-squares fitting using Equation (5) in the Supporting Information.

When changes in the fluorescence emission intensity at $\lambda = 535$ nm were plotted as a function of the concentration of IMP-1, a plateau was observed for concentrations of IMP-1 above 1 μM (Figure 2f). The apparent dissociation constants (K_d) of DansylC_nSHs with IMP-1 were estimated by nonlinear least-squares fitting of the titration data. The calculated K_d values were in the range of 67–975 nM (Table 1), indicating that DansylC₄SH binds to IMP-1 more tightly than the other DansylC_nSHs (for example, about 15-fold greater than DansylC₃SH). As determined from the dependence of the concentra-

Table 1. Dissociation and inhibition constants and IC₅₀ values for DansylC_nSHs ($n = 2-6$) toward IMP-1.

Compd	K_d [nM] ^[a]	K_i [nM] ^[b]	IC ₅₀ [μM] ^[b]
DansylC ₂ SH	356 ± 66	1100 ± 60	5.2 ± 0.4
DansylC ₃ SH	975 ± 110	1300 ± 100	6.3 ± 0.7
DansylC ₄ SH	67 ± 14	140 ± 10	0.7 ± 0.1
DansylC ₅ SH	154 ± 41	280 ± 10	1.6 ± 0.1
DansylC ₆ SH	105 ± 42	160 ± 10	1.0 ± 0.1

[a] Determined at 25 °C; for details, see Supporting Information. [b] Determined at 30 °C; for details, see Supporting Information.

tion of IMP-1 on the fluorescence emission intensity, all of the DansylC_nSHs bind to IMP-1 to form a 1:1 complex.

Previously, we reported that DansylC₂SH did not cause fluorescence enhancement in the presence of carbonic anhydrase, which contains a zinc(II) ion in the active site.^[18] This fluorescence enhancement was also not observed with other DansylC_nSHs ($n = 4-6$).

Considering the clinical applications of DansylC_nSHs, one of the major problems is whether DansylC_nSHs can be used to detect other MBLs. Therefore, we measured the fluorescence spectra of DansylC_nSHs in the presence of VIM-2. VIM-2, like IMP-1, is also extremely widespread. Although carbapenemase-producing organisms are rare in the United States, a nosocomial outbreak of pan-resistant *Pseudomonas aeruginosa* was reported recently,^[24] the strain expressed an integron-borne VIM-2. The Trp64 residue located at the top of loop 1 in IMP-1 is replaced by an alanine residue in VIM-2. This mutation is predicted to cause the fluorescence emission intensity to have different characteristics. Similar to IMP-1, the fluorescence emission intensity of DansylC_nSH increased with increasing concentrations of VIM-2 (see Supporting Information). However, the fluorescence intensity increases with the number of the methylene groups in the linker (i.e. DansylC₆SH showed a maximal fluorescence enhancement, with a K_d value of 190 nM; see Supporting Information). These results suggest that Trp64 in IMP-1 is an important factor in controlling the fluorescence properties of DansylC_nSH with MBLs.

We screened for inhibitory activity against IMP-1 from *Serratia marcescens* by measuring the initial velocity (v) against nitrocefin as a substrate in the presence of several concentrations of DansylC_nSHs. IC₅₀ (half-maximal inhibition) values were determined from a plot of fractional activity remaining against the concentration of DansylC_nSH (see Supporting Information). Moreover, the inhibition constant (K_i) for each DansylC_nSH was calculated according to a competitive inhibition pattern by fitting the kinetic data (see Supporting Information). The IC₅₀ and K_i values for IMP-1 were calculated to be 0.7–6.3 μM and 140–1300 nM, respectively. These results imply that the most potent inhibitor of IMP-1 was DansylC₄SH. In the case of VIM-2, the IC₅₀ and K_i values were calculated to be 1.5–3.4 μM and 286–720 nM, respectively (see Supporting Information).

The question of why DansylC₄SH exhibits the most fluorescence enhancement and inhibition among DansylC_nSHs is of interest. To address this, we prepared co-crystals of DansylC₄SH and IMP-1 to carry out an X-ray crystallographic analysis. The

X-ray crystal structure of the DansylC₄SH-IMP-1 complex was determined at a resolution of 2.43 Å by molecular replacement using the coordinates of IMP-1 (PDB code 1DD6).^[25] There were two molecules in an asymmetric unit, denoted as molecules A and B. The structure of the complex was refined to a final R_{working} value of 18.5% and an R_{free} value of 22.4% for data from 19.8 to 2.43 Å.^[26] Superposition of the α -carbon atoms of the two independent molecules A and B in the asymmetric unit gave a root-mean-square deviation (rmsd) of 0.35 Å.

The overall structure of each molecule adopts an $\alpha/\beta/\alpha$ sandwich structure, as is also found in native IMP-1 (Figure 3a).

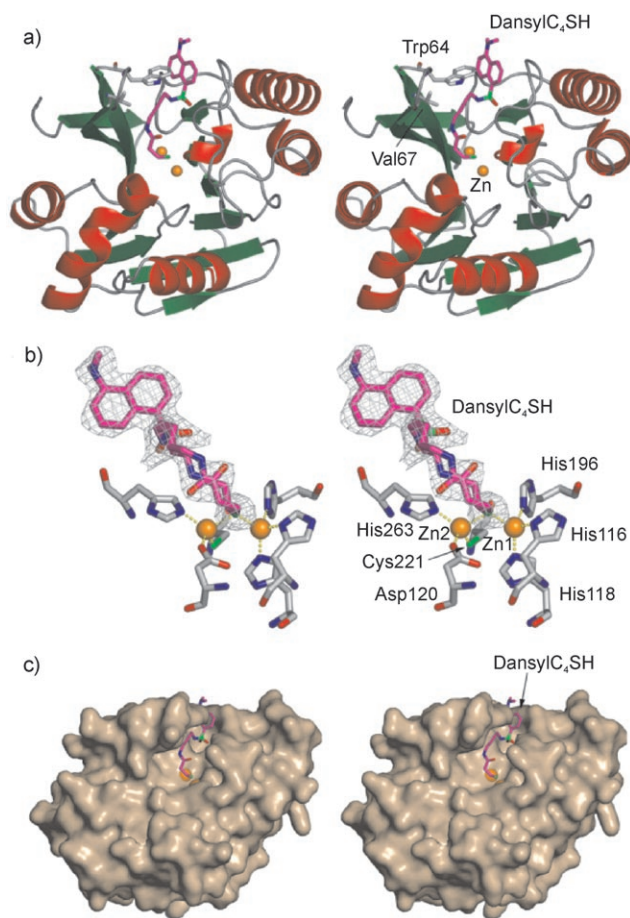


Figure 3. a) Overall structure of IMP-1 complexed with DansylC₄SH. DansylC₄SH has alternate conformations (Figure 3b) but herein, only one is represented. α Helices, β strands, and loops are shown in red, green, and gray, respectively. Zn^{II} atoms are shown as orange spheres. Carbon atoms in the DansylC₄SH are shown in violet. Trp64 and Val67 residues and DansylC₄SH are represented as sticks. Carbon atoms in Trp64 and Val67 residues are shown in gray (nitrogen = blue; oxygen = red; and sulfur = light green). b) The structure of the active site of IMP-1 complexed with DansylC₄SH. The electron density map (gray) of DansylC₄SH is shown contoured at the 2.5 σ level in the $F_o - F_c$ map. Zn^{II} atoms are shown as orange spheres. Carbon atoms of DansylC₄SH are shown in violet. His116, His118, His196, His263, Asp120, and Cys221 residues and DansylC₄SH are represented as sticks. Carbon atoms in His116, His118, His196, His263, Asp120, and Cys221 residues are shown in gray (nitrogen = blue; oxygen = red; and sulfur = light green). c) Molecular surface representation^[32] of IMP-1 complexed with DansylC₄SH. Zn^{II} atoms are shown as orange spheres. Carbon, nitrogen, oxygen, and sulfur atoms of DansylC₄SH are shown in violet, blue, red, and light green, respectively.

The DansylC₄SH-IMP-1 complex and native IMP-1 (PDB code 1DDK)^[25] were also superimposed, except for residues 62–65 which were disordered in native IMP-1, and the rmsd for C α between the complex and native IMP-1 was 0.52 Å for molecule A and 0.54 Å for molecule B. Glu60, Val61, and Val66, positioned on the base of a hairpin loop (residues 61–66, loop 1), confer flexibility near the active site. Asn185 is positioned in the other loop, which is exposed to solvent, and Asn233 and Gly235 are located in another loop (residues 221–241, loop 2) near the active site.

The active site of the DansylC₄SH-IMP-1 complex is shown in Figure 3b. As seen in the $F_o - F_c$ electron density map, a portion clearly alternates in the crystal and the two conformations fit the map very well, with the exception of the sulfonamide group of the naphthyl ring and the terminal thiol group in DansylC₄SH. Therefore, the corresponding atoms in the two conformations were refined with an occupancy of 0.5 in each case. The thiol group sulfur atom in DansylC₄SH bridges to two Zn^{II} ions (Zn1 and Zn2) with Zn1–S distances of 2.1 and 2.4 Å in molecules A and B, respectively, and with Zn2–S distances of 2.4 and 2.3 Å, respectively. Among the dinuclear Zn^{II} MBLs, a bridging H₂O or OH⁻ between Zn1 and Zn2 is thought to act as the attacking nucleophile on the carbonyl carbon atom of the β -lactam ring.^[27–29] The bridging H₂O or OH⁻ would be replaced with a sulfur atom of the thiol group in DansylC₄SH in the complex. This Zn^{II} coordination geometry is tetrahedral at both sites. On the other hand, in the case of native IMP-1, the coordination environment for the Zn2 site is proposed to have a disordered trigonal bipyramidal geometry occupied by a bridging H₂O or OH⁻, Cys221, and His263 in the equatorial positions, whereas Asp120 and the second H₂O occupy apical positions.^[25] The second H₂O is thought to contribute to the catalysis of the hydrolysis of β -lactams.^[30,31] It is proposed that the bridging of a thiol group to two Zn^{II} ions not only replaces a bridging H₂O or OH⁻ but also prevents H₂O from coordinating to the Zn2 site.

The naphthyl ring of DansylC₄SH is stabilized by a CH– π interaction (edge-to-face) with the indole ring of the Trp64 residue, leading to a change in the conformation of Trp64. The three-dimensional structure of IMP-1 complexed with the thio-carboxylate inhibitor 2-(5-(1-tetrazolymethyl)thien-3-yl)-N-(2-(thiomethyl)-4-(phenylbutyryl)glycine) has also been reported to have a similar interaction.^[25] In addition, the remaining portions between the naphthyl ring and a thiol group make hydrophobic contact with the Val61 residue (Figure 3a) and cover the shallow and wide active site cavity (Figure 3c).

Among the DansylC_nSHs, DansylC₄SH has an optimum length for binding to two Zn^{II} ions, replacing the bridging H₂O or OH⁻ that act as nucleophiles and the edge-to-face interaction with Trp64. The weakness of interaction between IMP-1 and other DansylC_nSHs may be due to steric hindrance or a lack of an attractive interaction between the enzyme, but further investigations for elucidating the relationships between structural and fluorescence properties are needed.

In conclusion, a series of dansyl derivatives, DansylC_nSHs ($n=2-6$), derived from *N*-(aminoalkyl)-5-dimethylaminonaphthalene-1-sulfonamide and 3-thiopropionic acid, were synthe-

sized in an attempt to develop a fluorescent probe for the detection of MBLs. DansylC₄SHs act not only as fluorescent probes, but also as inhibitors of IMP-1 and VIM-2. The three-dimensional structure of IMP-1 complexed with DansylC₄SH was determined; the main interactions occur between the naphthyl ring of the DansylC₄SH and Trp64 with an edge-to-face interaction, and the thiol group is coordinated to two Zn^{II} ions. These conclusions are also supported by fluorescence spectroscopy data. Thus, the spectral and structural data support the validity of our design strategy, which is aimed at developing both detection agents and inhibitors of MBLs. Finally, we expect that the fluorescent probes investigated in this study will serve as lead compounds for the further development of detection agents and specific high-affinity inhibitors that are selective for MBLs.

Acknowledgements

Work related to the preparation, purification, and inhibition studies of the enzymes was supported by a Grant from the Ministry of Health, Labor, and Welfare of Japan (H15-Shinkou-9). The synthetic, spectroscopic, and X-ray crystallographic studies were supported by a Grant-in-Aid for Scientific Research (B) (No. 16390017) from the Japanese Society for the Promotion of Science.

Keywords: bioinorganic chemistry · crystal structure analysis · fluorescent probes · inhibitors · metalloenzymes

- [1] K. Bush, M. Macielag, M. Weidner-Wells, *Curr. Opin. Microbiol.* **2004**, *7*, 466–476.
- [2] C. J. Thomson, E. Power, H. Ruebsamen-Waigmann, H. Labischinski, *Curr. Opin. Microbiol.* **2004**, *7*, 445–450.
- [3] D. Payne, A. Tomasz, *Curr. Opin. Microbiol.* **2004**, *7*, 435–438.
- [4] F. M. Walsh, S. G. Amyes, *Curr. Opin. Microbiol.* **2004**, *7*, 439–444.
- [5] J. M. Thomson, R. A. Bonomo, *Curr. Opin. Microbiol.* **2005**, *8*, 518–524.
- [6] U. Heinz, H. W. Adolph, *Cell. Mol. Life Sci.* **2004**, *61*, 2827–2839.
- [7] M. S. Helfand, R. A. Bonomo, *Curr. Opin. Pharmacol.* **2005**, *5*, 452–458.
- [8] J. F. Fisher, S. O. Meroueh, S. Mobashery, *Chem. Rev.* **2005**, *105*, 395–424.
- [9] T. R. Walsh, M. A. Toleman, L. Poirel, P. Nordmann, *Clin. Microbiol. Rev.* **2005**, *18*, 306–325.
- [10] R. P. Ambler, *Philos. Trans. R. Soc. London Ser. B* **1980**, *289*, 321–331.
- [11] M. Galleni, J. Lamotte-Brasseur, G. M. Rossolini, J. Spencer, O. Dideberg, J.-M. Frère, *Antimicrob. Agents Chemother.* **2001**, *45*, 660–663.
- [12] K. Bush, G. A. Jacoby, A. A. Medeiros, *Antimicrob. Agents Chemother.* **1995**, *39*, 1211–1233.
- [13] Y. Arakawa, M. Murakami, K. Suzuki, H. Ito, R. Wacharotayankun, S. Ohsuka, N. Kato, M. Ohta, *Antimicrob. Agents Chemother.* **1995**, *39*, 1612–1615.
- [14] G. Cornaglia, M. L. Riccio, A. Mazzariol, L. Lauretti, R. Fontana, G. M. Rossolini, *Lancet* **1999**, *353*, 899–900.
- [15] J. Spencer, T. R. Walsh, *Angew. Chem.* **2006**, *118*, 1038–1042; *Angew. Chem. Int. Ed.* **2006**, *45*, 1022–1026.
- [16] M. Goto, T. Takahashi, F. Yamashita, A. Koreeda, H. Mori, M. Ohta, Y. Arakawa, *Biol. Pharm. Bull.* **1997**, *20*, 1136–1140.
- [17] H. Kurosaki, Y. Yamaguchi, T. Higashi, K. Soga, S. Matsueda, H. Yumoto, S. Misumi, Y. Yamagata, Y. Arakawa, M. Goto, *Angew. Chem.* **2005**, *117*, 3929–3932; *Angew. Chem. Int. Ed.* **2005**, *44*, 3861–3864.
- [18] H. Kurosaki, H. Yasuzawa, Y. Yamaguchi, W. Jin, Y. Arakawa, M. Goto, *Org. Biomol. Chem.* **2003**, *1*, 17–20.
- [19] L. Poirel, T. Naas, D. Nicolas, L. Collet, S. Bellais, J.-D. Cavallo, P. Nordmann, *Antimicrob. Agents Chemother.* **2000**, *44*, 891–897.
- [20] J.-J. Yan, W.-C. Ko, J.-J. Wu, *Antimicrob. Agents Chemother.* **2001**, *45*, 2368–2371.
- [21] M. L. Riccio, N. Franceschini, L. Boschi, B. Caravelli, G. Cornaglia, R. Fontana, G. Amicosante, G. M. Rossolini, *Antimicrob. Agents Chemother.* **2000**, *44*, 1229–1235.
- [22] S. Iyobe, H. Kusadokoro, J. Ozaki, N. Matsumura, S. Minami, S. Haruta, T. Sawai, K. O'Hara, *Antimicrob. Agents Chemother.* **2000**, *44*, 2023–2027.
- [23] Y.-W. Chu, M. Afzal-Shah, E. T. S. Houang, M.-F. I. Palepou, D. J. Lyon, N. Woodford, D. M. Livermore, *Antimicrob. Agents Chemother.* **2001**, *45*, 710–714.
- [24] K. Lolans, A. M. Queenan, K. Bush, A. Sahud, J. P. Quinn, *Antimicrob. Agents Chemother.* **2005**, *49*, 3538–3540.
- [25] N. O. Concha, C. A. Janson, P. Rowling, S. Pearson, C. A. Cheever, B. P. Clarke, C. Lewis, M. Galleni, J.-M. Frère, D. J. Payne, J. H. Bateson, S. S. Abdel-Meguid, *Biochemistry* **2000**, *39*, 4288–4298.
- [26] The atomic coordinates of IMP-1, when complexed with DasyI4SH have been deposited in the Protein Data Bank with the following accession code: 2DOO.
- [27] N. O. Concha, B. A. Rasmussen, K. Bush, O. Herzberg, *Structure* **1996**, *4*, 823–836.
- [28] J. H. Ullah, T. R. Walsh, I. A. Taylor, D. C. Emery, C. S. Verma, S. J. Gamblin, J. Spencer, *J. Mol. Biol.* **1998**, *284*, 125–136.
- [29] Z. Wang, W. Fast, A. M. Valentine, S. J. Benkovic, *Curr. Opin. Chem. Biol.* **1999**, *3*, 614–622.
- [30] M. P. Yanchak, R. A. Taylor, M. W. Crowder, *Biochemistry* **2000**, *39*, 11330–11339.
- [31] J. D. Garrity, A. L. Carenbauer, L. R. Herron, M. W. Crowder, *J. Biol. Chem.* **2004**, *279*, 920–927.
- [32] A. Nicholls, GRASP, Graphical Representation and Analysis of Surface Properties, Columbia University, New York, **1992**.

Received: May 6, 2006

Published online on August 28, 2006